OM of: US-09-126-945B-2_COPY_2_335 to: N_Geneseq_0601:* out_format : pfs

Date: Sep 7, 2001 6:30 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09126945/runat_07092001_152109_3686/app_query.fasta_1.487
-DB=N_Geneseq_0601 -QFMT=fastap -SUFFIX=olig.rng -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=US09126945_@CGN1_1_300 -NCPU=6 -ICPU=3
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT
-THREADS=1

Search information block:
Query: US-09-126-945B-2_COPY_2_335
Query length: 334
Database: N_Geneseq_0601:*
Database sequences: 730101
Database length: 313950809
Search time (sec): 104.390000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:

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/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ50691	+	334.00	5893.13	0.0	1894				
/SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC83261	+	334.00	5893.13	0.0	1894				
/SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC83266	+	334.00	5888.88	0.0	3317				
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAF21828	+	248.00	4372.45	1.4e-235	1087				
/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA06617	+	80.00	1403.94	3.1e-70	278				
/SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ91769	+	14.00	219.50	0.0003	1800				
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/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ50016	+	14.00	218.46	0.0003	2064				
/SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ55149	+	14.00	218.43	0.0003	2073				
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/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ50015	+	14.00	217.29	0.0004	2410				
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/SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC99029	+	14.00	215.75	0.0005	2952				
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/SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV89617	+	9.00	145.50	3.92	261				
/SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ81001	+	9.00	137.72	10.61	727				
/SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ66045	+	9.00	129.21	31.62	2233				
/SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ68555	+	9.00	126.25	46.21	3298				
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/SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV64836	-	8.00	129.71	29.67	202				
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seq_documentation_block:

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ID   AAZ50691 standard; cDNA; 1894 BP.
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AC   AAZ50691;
XX
DT   23-MAY-2000  (first entry)
XX
DE   Human prostate derived Ets factor cDNA.
XX
KW   Prostate Derived Ets factor; PDEF; human; chromosome 6p21.3; cancer;
KW   loss of heterozygosity; chromosomal translocation; linkage analysis;
KW   cytostatic; cardiant; immunosuppressive; cerebroprotective; fungicide;
KW   antibacterial; vulnerary; neuroprotective; antiparkinsonian; nootropic;
KW   anabolic; antiinflammatory; anorectic; hybridisation probe; forensic;
KW   tumour marker; diagnosis; treatment; prostate cancer; blood coagulation;
KW   autoimmune disorder; haematopoietic; immune/nervous system; stroke;
KW   neoplasm; microbial infection; tissue regeneration; heart attack;
KW   scarring; food additive; preservative; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             416..1423
FT                   /*tag= a
FT                   /product= "Human prostate derived Ets factor"
FT                   /note= "Expressed in prostate epithelium"
XX
PN   WO200006589-A1.
XX
PD   10-FEB-2000.
XX
PF   02-AUG-1999;   99WO-US17470.
XX
PR   31-JUL-1998;   98US-0126945.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI   Libermann TA,  Oettgen JP,  Kunsch CA,  Endress GA,  Rosen CA;
XX
DR   WPI; 2000-195255/17.
DR   P-PSDB; AAY45003.
XX
PT   Novel prostate derived polypeptide, polynucleotide useful for
PT   diagnosis, prevention and treatment of prostate cancer, autoimmune
PT   disorders, microbial infections and also as food additive or
PT   preservative  -
XX
PS   Claim 4; Fig 1; 132pp; English.
XX
CC   The present cDNA sequence encodes a human prostate derived Ets factor
CC   (PDEF), isolated from human prostate carcinoma cDNA library
CC   (ATCC No.203072). PDEF gene expression is highest in tissues involved in
CC   androgen sensitivity, with enriched expression in prostate epithelium
CC   cells. PDEF gene is mapped to the human chromosome 6p21.3
CC   region that is associated with loss of heterozygosity and chromosomal
CC   translocations in various human cancers. PDEF has cytostatic, cardiant,
CC   immunosuppressive, cerebroprotective, fungicide, antibacterial,
CC   vulnerary, neuroprotective, antiparkinsonian, nootropic, anabolic,
CC   antiinflammatory and anorectic activity. PDEF polynucleotides are useful
CC   in linkage analysis as markers, as hybridisation probes for differential
CC   identification of the tissues or cell types and as polymorphic markers
CC   for forensic purposes. PDEF is useful as prostate-specific tumour marker
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CC   for the diagnosis and treatment of prostate cancer. PDEF sequences are
CC   useful for treating autoimmune disorders, haematopoietic, blood
CC   coagulation, immune and nervous system disorders, hyperproliferative
CC   disorders like, neoplasms and microbial infections, heart attacks,
CC   stroke, scarring and for tissue regeneration. They are also useful as
CC   food additives or preservatives.
XX
SQ   Sequence 1894 BP; 368 A; 653 C; 571 G; 302 T; 0 other;

alignment_scores:
            Quality:  334.00              Length:    334
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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      17 uProProAspThrValSerArgThrGlyLeuGluLysAlaAlaAlaGlyA 34
         |||||||||||||||||||||||||||||||||||||||||||||||||
     469 GCCCCCCGACACGGTGTCGCGGACAGGCTTGGAGAAGGCGGCAGCGGGGG 518

      34 laValGlyLeuGluArgArgAspTrpSerProSerProProAlaThrPro 50
         |||||||||||||||||||||||||||||||||||||||||||||||||
     519 CAGTGGGTCTCGAGAGACGGGACTGGAGTCCCAGTCCACCCGCCACGCCC 568

      51 GluGlnGlyLeuSerAlaPheTyrLeuSerTyrPheAspMetLeuTyrPr 67
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     569 GAGCAGGGCCTGTCCGCCTTCTACCTCTCCTACTTTGACATGCTGTACCC 618

      67 oGluAspSerSerTrpAlaAlaLysAlaProGlyAlaSerSerArgGluG 84
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     619 TGAGGACAGCAGCTGGGCAGCCAAGGCCCCTGGGGCCAGCAGTCGGGAGG 668

      84 luProProGluGluProGluGlnCysProValIleAspSerGlnAlaPro 100
         |||||||||||||||||||||||||||||||||||||||||||||||||
     669 AGCCACCTGAGGAGCCTGAGCAGTGCCCGGTCATTGACAGCCAAGCCCCA 718

     101 AlaGlySerLeuAspLeuValProGlyGlyLeuThrLeuGluGluHisSe 117
         |||||||||||||||||||||||||||||||||||||||||||||||||
     719 GCGGGCAGCCTGGACTTGGTGCCCGGCGGGCTGACCTTGGAGGAGCACTC 768

     117 rLeuGluGlnValGlnSerMetValValGlyGluValLeuLysAspIleG 134
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     819 AGACGGCCTGCAAGCTGCTCAACATCACCGCAGATCCCATGGACTGGAGC 868

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     184 laMetSerGluGluGlnPheArgGlnArgSerProLeuGlyGlyAspVal 200
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     201 LeuHisAlaHisLeuAspIleTrpLysSerAlaAlaTrpMetLysGluAr 217
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     217 gThrSerProGlyAlaIleHisTyrCysAlaSerThrSerGluGluSerT 234
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    1069 GACTTCACCTGGGGCGATTCACTACTGTGCCTCGACCAGTGAGGAGAGCT 1118

     234 rpThrAspSerGluValAspSerSerCysSerGlyGlnProIleHisLeu 250
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     251 TrpGlnPheLeuLysGluLeuLeuLeuLysProHisSerTyrGlyArgPh 267
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     267 eIleArgTrpLeuAsnLysGluLysGlyIlePheLysIleGluAspSerA 284
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    1319 TACGACAAGCTGAGCCGCTCCATCCGCCAGTATTACAAGAAGGGCATCAT 1368

     317 eArgLysProAspIleSerGlnArgLeuValTyrGlnPheValHisProI 334
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC83261

seq_documentation_block:
ID   AAC83261 standard; DNA; 1894 BP.
XX
AC   AAC83261;
XX
DT   16-MAR-2001  (first entry)
XX
DE   Gland-specific Ets transcription factor (GSEF) nucleotide sequence.
XX
KW   Transcription factor; gland-specific Ets transcription factor; GSEF;
KW   metastatic potential; cancer; tumour; metastasis; breast; prostate;
KW   leukaemia; lymphoma; sarcoma; melanoma; chromosome 6p21.1-6p21.3; ds.
XX
OS   Homo sapiens.
XX
PN   WO200070092-A1.
XX
PD   23-NOV-2000.
XX
PF   12-MAY-2000; 2000WO-US13173.
XX
PR   14-MAY-1999;   99US-0134112.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Kaufmann J,  Xin H,  Harrowe G;
XX
DR   WPI; 2001-041019/05.
DR   P-PSDB; AAB49628.
XX
PT   Detecting metastatic and potential metastatic cancerous cells, useful
PT   for diagnosing, prognosing, grading and staging of cancers by detecting
PT   gland-specific Ets transcription factor gene product in a biological
PT   sample from a cell  -
XX
PS   Disclosure; Page 81-83; 95pp; English.
XX
CC   This invention relates to a method for the detection and determination of
CC   the metastatic potential of a cell. The method comprises detecting a
CC   gland-specific Ets transcription factor (GSEF) gene product in a test
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CC   sample. Detection of a GSEF gene product in the test sample in amount
CC   lower than that in a normal cell, is indicative of a cell with high
CC   metastatic potential. The method is useful for determining the metastatic
CC   potential of a cell, for the diagnosis and prognosis of cancer as well as
CC   grading and staging of cancers by detecting GSEF expression in a
CC   biological test sample. The method may also be used to monitor patients
CC   having a predisposition to develop a particular cancer. GSEF polypeptides
CC   are useful for producing antibodies, in cancer diagnosis, prognosis,
CC   grading, staging and management of breast and prostate tumours, and in
CC   detecting polymorphisms in the sequence. GSEF genes and proteins are also
CC   useful in gene therapy. GSEF gene product expression levels can be used
CC   in conjunction with any tissue in which an alteration in GSEF gene
CC   product expression levels is associated with development of a
CC   cancer-associated phenotype. Cancers, which can be monitored include
CC   cancers of the prostate, cervix, lung and colon, melanomas, colorectal
CC   adenocarcinomas, Wilm's tumour, retinoblastoma, sarcomas, myosarcomas,
CC   lung carcinomas, leukaemia, and lymphomas. The GSEF gene is located on
CC   human chromosome 6, specifically at 6p21.1-6p21.3. The present sequence
CC   represents the DNA encoding GSEF.
XX
SQ   Sequence 1894 BP; 368 A; 653 C; 571 G; 302 T; 0 other;


alignment_scores:
            Quality:  334.00              Length:    334
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAC83261   ..

 Align seg 1/1  to: AAC83261  from: 1  to: 1894

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      17 uProProAspThrValSerArgThrGlyLeuGluLysAlaAlaAlaGlyA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     469 GCCCCCCGACACGGTGTCGCGGACAGGCTTGGAGAAGGCGGCAGCGGGGG 518

      34 laValGlyLeuGluArgArgAspTrpSerProSerProProAlaThrPro 50
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     519 CAGTGGGTCTCGAGAGACGGGACTGGAGTCCCAGTCCACCCGCCACGCCC 568

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     619 TGAGGACAGCAGCTGGGCAGCCAAGGCCCCTGGGGCCAGCAGTCGGGAGG 668

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     669 AGCCACCTGAGGAGCCTGAGCAGTGCCCGGTCATTGACAGCCAAGCCCCA 718

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     719 GCGGGCAGCCTGGACTTGGTGCCCGGCGGGCTGACCTTGGAGGAGCACTC 768

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     969 CCATGTCGGAGGAGCAGTTCCGCCAGCGCTCGCCCCTGGGTGGGGATGTG 1018

     201 LeuHisAlaHisLeuAspIleTrpLysSerAlaAlaTrpMetLysGluAr 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1019 CTGCACGCCCACCTGGACATCTGGAAGTCAGCGGCCTGGATGAAAGAGCG 1068

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1069 GACTTCACCTGGGGCGATTCACTACTGTGCCTCGACCAGTGAGGAGAGCT 1118

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         ||||||||||||||||||||||||||||||||||||||||||||||||||
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     251 TrpGlnPheLeuLysGluLeuLeuLeuLysProHisSerTyrGlyArgPh 267
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC83266

seq_documentation_block:
ID   AAC83266 standard; DNA; 3317 BP.
XX
AC   AAC83266;
XX
DT   16-MAR-2001  (first entry)
XX
DE   Gland-specific Ets transcription factor (GSEF) cDNA sequence.
XX
KW   Transcription factor; gland-specific Ets transcription factor; GSEF;
KW   metastatic potential; cancer; tumour; metastasis; breast; prostate;
KW   leukaemia; lymphoma; sarcoma; melanoma; chromosome 6p21.1-6p21.3; ss.
XX
OS   Homo sapiens.
XX
PN   WO200070092-A1.
XX
PD   23-NOV-2000.
XX
PF   12-MAY-2000; 2000WO-US13173.
XX
PR   14-MAY-1999;   99US-0134112.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Kaufmann J,  Xin H,  Harrowe G;
XX
```

```
DR   WPI; 2001-041019/05.
DR   P-PSDB; AAB49633.
XX
PT   Detecting metastatic and potential metastatic cancerous cells, useful
PT   for diagnosing, prognosing, grading and staging of cancers by detecting
PT   gland-specific Ets transcription factor gene product in a biological
PT   sample from a cell  -
XX
PS   Disclosure; Fig 2; 95pp; English.
XX
CC   This invention relates to a method for the detection and determination of
CC   the metastatic potential of a cell. The method comprises detecting a
CC   gland-specific Ets transcription factor (GSEF) gene product in a test
CC   sample. Detection of a GSEF gene product in the test sample in amount
CC   lower than that in a normal cell, is indicative of a cell with high
CC   metastatic potential. The method is useful for determining the metastatic
CC   potential of a cell, for the diagnosis and prognosis of cancer as well as
CC   grading and staging of cancers by detecting GSEF expression in a
CC   biological test sample. The method may also be used to monitor patients
CC   having a predisposition to develop a particular cancer. GSEF polypeptides
CC   are useful for producing antibodies, in cancer diagnosis, prognosis,
CC   grading, staging and management of breast and prostate tumours, and in
CC   detecting polymorphisms in the sequence. GSEF genes and proteins are also
CC   useful in gene therapy. GSEF gene product expression levels can be used
CC   in conjunction with any tissue in which an alteration in GSEF gene
CC   product expression levels is associated with development of a
CC   cancer-associated phenotype. Cancers, which can be monitored include
CC   cancers of the prostate, cervix, lung and colon, melanomas, colorectal
CC   adenocarcinomas, Wilm's tumour, retinoblastoma, sarcomas, myosarcomas,
CC   lung carcinomas, leukaemia, and lymphomas. The GSEF gene is located on
CC   human chromosome 6, specifically at 6p21.1-6p21.3. The present sequence
CC   represents the cDNA encoding GSEF.
XX
SQ   Sequence 3317 BP; 710 A; 1026 C; 970 G; 611 T; 0 other;

alignment_scores:
            Quality:  334.00              Length:    334
              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: AAC83266  from: 1  to: 3317

       1 GlySerAlaSerProGlyLeuSerSerValSerProSerHisLeuLeLe 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1818 GGCAGCGCCAGCCCGGGTCTGAGCAGCGTATCCCCCAGCCACCTCCTGCT 1867

      17 uProProAspThrValSerArgThrGlyLeuGluLysAlaAlaAlaGlyA 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1868 GCCCCCCGACACGGTGTCGCGGACAGGCTTGGAGAAGGCGGCAGCGGGGG 1917

      34 laValGlyLeuGluArgArgAspTrpSerProSerProProAlaThrPro 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1918 CAGTGGGTCTCGAGAGACGGGACTGGAGTCCCAGTCCACCCGCCACGCCC 1967

      51 GluGlnGlyLeuSerAlaPheTyrLeuSerTyrPheAspMetLeuTyrPr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1968 GAGCAGGGCCTGTCCGCCTTCTACCTCTCCTACTTTGACATGCTGTACCC 2017

      67 oGluAspSerSerTrpAlaAlaLysAlaProGlyAlaSerSerArgGluG 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2018 TGAGGACAGCAGCTGGGCAGCCAAGGCCCCTGGGGCCAGCAGTCGGGAGG 2067

      84 luProProGluGluProGluGlnCysProValIleAspSerGlnAlaPro 100
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2068 AGCCACCTGAGGAGCCTGAGCAGTGCCCGGTCATTGACAGCCAAGCCCCA 2117

     101 AlaGlySerLeuAspLeuValProGlyGlyLeuThrLeuGluGluHisSe 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2118 GCGGGCAGCCTGGACTTGGTGCCCGGCGGGCTGACCTTGGAGGAGCACTC 2167

     117 rLeuGluGlnValGlnSerMetValValGlyGluValLeuLysAspIleG 134
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2168 GCTGGAGCAGGTGCAGTCCATGGTGGTGGGCGAAGTGCTCAAGGACATCG 2217

     134 luThrAlaCysLysLeuLeuAsnIleThrAlaAspProMetAspTrpSer 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2218 AGACGGCCTGCAAGCTGCTCAACATCACCGCAGATCCCATGGACTGGAGC 2267

     151 ProSerAsnValGlnLysTrpLeuLeuTrpThrGluHisGlnTyrArgLe 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2268 CCCAGCAATGTGCAGAAGTGGCTCCTGTGGACAGAGCACCAATACCGGCT 2317

     167 uProProMetGlyLysAlaPheGlnGluLeuAlaGlyLysGluLeuCysA 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2318 GCCCCCCATGGGCAAGGCCTTCCAGGAGCTGGCGGGCAAGGAGCTGTGCG 2367

     184 laMetSerGluGluGlnPheArgGlnArgSerProLeuGlyGlyAspVal 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2368 CCATGTCGGAGGAGCAGTTCCGCCAGCGCTCGCCCCTGGGTGGAGATGTG 2417

     201 LeuHisAlaHisLeuAspIleTrpLysSerAlaAlaTrpMetLysGluAr 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2418 CTGCACGCCCACCTGGACATCTGGAAGTCAGCGGCCTGGATGAAAGAGCG 2467

     217 gThrSerProGlyAlaIleHisTyrCysAlaSerThrSerGluGluSerT 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2468 GACTTCACCTGGGGCGATTCACTACTGTGCCTCGACCAGTGAGGAGAGCT 2517

     234 rpThrAspSerGluValAspSerSerCysSerGlyGlnProIleHisLeu 250
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2518 GGACCGACAGCGAGGTGGACTCATCATGCTCCGGGCAGCCCATCCACCTG 2567

     251 TrpGlnPheLeuLysGluLeuLeuLeuLysProHisSerTyrGlyArgPh 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2568 TGGCAGTTCCTCAAGGAGTTGCTACTCAAGCCCCACAGCTATGGCCGCTT 2617

     267 eIleArgTrpLeuAsnLysGluLysGlyIlePheLysIleGluAspSerA 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2618 CATTAGGTGGCTCAACAAGGAGAAGGGCATCTTCAAAATTGAGGACTCAG 2667

     284 laGlnValAlaArgLeuTrpGlyIleArgLysAsnArgProAlaMetAsn 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2668 CCCAGGTGGCCCGGCTGTGGGGCATCCGCAAGAACCGTCCCGCCATGAAC 2717

     301 TyrAspLysLeuSerArgSerIleArgGlnTyrTyrLysGlyIleIl 317
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2718 TACGACAAGCTGAGCCGCTCCATCCGCCAGTATTACAAGAAGGGCATCAT 2767

     317 eArgLysProAspIleSerGlnArgLeuValTyrGlnPheValHisProI 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    2768 CCGGAAGCCAGACATCTCCCAGCGCCTCGTCTACCAGTTCGTGCACCCCA 2817

     334 le 334
         ||
    2818 TC 2819

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAF21828

seq_documentation_block:
ID   AAF21828 standard; DNA; 1087 BP.
XX
AC   AAF21828;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 215.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
KW   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW   antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
```

```
KW   autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW   multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW   cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200055173-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05881.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-611515/58.
DR   P-PSDB; AAB58925.
XX
PT   New human breast and ovarian cancer associated gene sequences and the
PT   polypeptides encoded by these genes, useful in the prevention,
PT   treatment and diagnosis of cancer, immune disorders, cardiovascular
PT   disorders and neurological diseases -
XX
PS   Claim 1; Page 642-643; 1299pp; English.
XX
CC   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC   proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive;
CC   nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
CC   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
CC   antibacterial; antifungal; antiparasitic and cardiant activity. The
CC   polynucleotide and protein sequences are used in the diagnosis of cancer,
CC   particularly breast and ovarian cancer. The nucleic acid sequences,
CC   proteins, agonists and agonists may also be used in the diagnosis,
CC   prevention and treatment of immune disorders e.g. Addison's disease,
CC   allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC   diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC   arthritis and ulcerative colitis; cardiovascular disorders such as
CC   myocardial ischaemias; wound healing; neurological diseases such as
CC   cerebral anoxia and epilepsy; and infectious diseases.
XX
SQ   Sequence 1087 BP; 215 A; 347 C; 339 G; 182 T; 4 other;

alignment_scores:
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              Ratio:  1.000                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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      42 TrpSerProSerProProAlaThrProGluGlnGlyLeuSerAlaPheTy 58
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       3 TGGAGTCCCAGTCCACCCGCCACGCCCGAGCAGGGCCTGTCCGCCTTCTA 52

      58 rLeuSerTyrPheAspMetLeuTyrProGluAspSerSerTrpAlaAlaL 75
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      53 CCTCTCCTACTTTGACATGCTGTACCCTGAGGACAGCAGCTGGGCAGCCA 102

      75 ysAlaProGlyAlaSerSerArgGluGluProProGluGluProGluGln 91
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     103 AGGCCCCTGGGGCCAGCAGTCGGGAGGAGCCACCTGAGGAGCCTGAGCAG 152

      92 CysProValIleAspSerGlnAlaProAlaGlySerLeuAspLeuValPr 108
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     153 TGCCCGGTCATTGACAGCCAAGCCCCAGCGGGCAGCCTGGACTTGGTGCC 202

     108 oGlyGlyLeuThrLeuGluGluHisSerLeuGluGlnValGlnSerMetV 125
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     203 CGGCGGGCTGACCTTGGAGGAGCACTCGCTGGAGCAGGTGCAGTCCATGG 252

     125 alValGlyGluValLeuLysAspIleGluThrAlaCysLysLeuLeuAsn 141
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     253 TGGTGGGCGAAGTGCTCAAGGACATCGAGACGGCCTGCAAGCTGCTCAAC 302

     142 IleThrAlaAspProMetAspTrpSerProSerAsnValGlnLysTrpLe 158
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     303 ATCACCGCAGATCCCATGGACTGGAGCCCCAGCAATGTGCAGAAGTGGCT 352

     158 uLeuTrpThrGluHisGlnTyrArgLeuProProMetGlyLysAlaPheG 175
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     353 CCTGTGGACAGAGCACCAATACCGGCTGCCCCCCATGGGCAAGGCCTTCC 402

     175 lnGluLeuAlaGlyLysGluLeuCysAlaMetSerGluGluGlnPheArg 191
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     403 AGGAGCTGGCGGGCAAGGAGCTGTGCGCCATGTCGGAGGAGCAGTTCCGC 452

     192 GlnArgSerProLeuGlyGlyAspValLeuHisAlaHisLeuAspIleTr 208
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     453 CAGCGCTCGCCCCTGGGTGGGGATGTGCTGCACGCCCACCTGGACATCTG 502

     208 pLysSerAlaAlaTrpMetLysGluArgThrSerProGlyAlaIleHisT 225
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     503 GAAGTCAGCGGCCTGGATGAAAGAGCGGACTTCACCTGGGGCGATTCACT 552

     225 yrCysAlaSerThrSerGluGluSerTrpThrAspSerGluValAspSer 241
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     553 ACTGTGCCTCGACCAGTGAGGAGAGCTGGACCGACAGCGAGGTGGACTCA 602

     242 SerCysSerGlyGlnProIleHisLeuTrpGlnPheLeuLysGluLeuLe 258
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     603 TCATGCTCCGGGCAGCCCATCCACCTGTGGCAGTTCCTCAAGGAGTTGCT 652

     258 uLeuLysProHisSerTyrGlyArgPheIleArgTrpLeuAsnLysGluL 275
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     653 ACTCAAGCCCCACAGCTATGGCCGCTTCATTAGGTGGCTCAACAAGGAGA 702

     275 ysGlyIlePheLysIleGluAspSerAlaGlnValAlaArgLeu 289
         |||||||||||||||||||||||||||||||||||||||||||||
     703 AGGGCATCTTCAAAATTGAGGACTCAGCCCAGGTGGCCCGGCTG 746

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA06617

seq_documentation_block:
ID   AAA06617 standard; cDNA; 278 BP.
XX
AC   AAA06617;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:398.
XX
KW   Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW   immunogenic; cytostatic; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200004149-A2.
XX
PD   27-JAN-2000.
XX
PF   14-JUL-1999;   99WO-US15838.
XX
PR   14-JUL-1998;   98US-0115453.
PR   14-JUL-1998;   98US-0116134.
PR   23-SEP-1998;   98US-0159812.
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PR   23-SEP-1998;   98US-0159822.
PR   15-JAN-1999;   99US-0232149.
PR   15-JAN-1999;   99US-0232880.
PR   09-APR-1999;   99US-0288946.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Dillon DC,  Harlocker SL,  Yuqiu J,  Xu J,  Mitcham JL;
XX
DR   WPI; 2000-171268/15.
XX
PT   New polypeptide useful for treating and diagnosing prostate cancer
PT   comprises an immunogenic portion of prostate tumor protein -
XX
PS   Claim 50; Page 239; 263pp; English.
XX
CC   The present invention describes isolated polypeptides, comprising an
CC   immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC   and polynucleotides encoding them have cytostatic activity and can be
CC   used in vaccines and in gene therapy. The polypeptides and
CC   polynucleotides encoding them, antigen presenting cells which express
CC   the polypeptides, antibodies against the polypeptides and vaccines
CC   comprising them can be used for inhibiting the development of prostate
CC   cancer in a patient. The polypeptides can be used to generate antibodies
CC   or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC   the polynucleotides encoding the polypeptides can be used as a probe or
CC   to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC   AAY82000 to AAY82020 represent sequences used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 278 BP; 56 A; 85 C; 87 G; 49 T; 1 other;


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             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

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     189 GlnPheArgGlnArgSerProLeuGlyGlyAspValLeuHisAlaHisLe 205
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      17 CAGTTCCGCCAGCGCTCGCCCCTGGGTGGGGATGTGCTGCACGCCCACCT 66

     205 uAspIleTrpLysSerAlaAlaTrpMetLysGluArgThrSerProGlyA 222
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      67 GGACATCTGGAAGTCAGCGGCCTGGATGAAAGAGCGGACTTCACCTGGGG 116

     222 laIleHisTyrCysAlaSerThrSerGluGluSerTrpThrAspSerGlu 238
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     117 CGATTCACTACTGTGCCTCGACCAGTGAGGAGAGCTGGACCGACAGCGAG 166

     239 ValAspSerSerCysSerGlyGlnProIleHisLeuTrpGlnPheLeuLy 255
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     167 GTGGACTCATCATGCTCCGGGCAGCCCATCCACCTGTGGCAGTTCCTCAA 216

     255 sGluLeuLeuLeuLysProHisSerTyrGlyArgPheIle 268
         |||||||||||||||||||||||||||||||||||||||
     217 GGAGTTGCTACTCAAGCCCCACAGCTATGGCCGCTTCATT 256

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:AAQ91769

seq_documentation_block:
ID   AAQ91769 standard; cDNA to mRNA; 1800 BP.
XX
AC   AAQ91769;
XX
DT   09-FEB-1996  (first entry)
XX
DE   Coding sequence of PEA3-beta, an ETS transcription factor.
XX
KW   Transcription factor; probe; reverse transcription; PCR; primer;
KW   expression vector; E.coli; COS cell; ras; cancer cell multiplication;
KW   polyoma virus; transformation; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1563
FT                   /*tag= a
FT                   /product= PEA3-beta transcription factor
FT   CDS             250..252
FT                   /*tag= b
FT                   /transl_except= seq: CTC  a.a.:Pro
FT   CDS             376..378
FT                   /*tag= c
FT                   /transl_except= seq: AAC  a.a.: Lys
FT   CDS             1498..1500
FT                   /*tag= d
FT                   /transl_except= seq: ACC  a.a.: Ser
XX
PN   JP07145197-A.
XX
PD   06-JUN-1995.
XX
PF   25-NOV-1993;   93JP-0295393.
XX
PR   25-NOV-1993;   93JP-0295393.
XX
PA   (EISA ) EISAI CO LTD.
PA   (HIRA/) HIRANO T.
XX
DR   WPI; 1995-237197/31.
DR   P-PSDB; AAR78185.
XX
PT   ETS transcription factor activated by ras - may be used in the study
PT   of cancer cell proliferation and the proliferation of the polyoma
PT   virus
XX
PS   Claim 2; Page 7-9; 9pp; Japanese.
XX
CC   The nucleotide sequence of the novel ETS transcription factor family
CC   member - PEA3-beta.  The gene was isolated from a HepG2 cell line cDNA
CC   library.  The probe for the screening was prepared by reverse
CC   transcription on HepG2 mRNA followed by PCR using primers AAQ91770-1,
CC   to produce a probe of 170-200 bp.  The screening isolated the full
CC   length sequence of the transcription factor.  The gene was inserted into
CC   the expression vectors pBluescript KS and pcDV1 for expression of the
CC   protein in E.coli and COS7 cells, respectively.  The ETS transcription
CC   factor has specificity for and is activated by ras. It is useful as a
CC   reagent in studies for the elucidation of the mechanism of cancer cell
CC   multiplication or polyoma virus transformation of cells.
XX
SQ   Sequence 1800 BP; 437 A; 522 C; 435 G; 405 T; 1 other;


alignment_scores:
           Quality:   14.00              Length:     14
             Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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 Align seg 1/1  to: AAQ91769  from: 1  to: 1800

     294 LysAsnArgProAlaMetAsnTyrAspLysLeuSerArgSer 307
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    1234 AAGAACCGGCCAGCCATGAACTATGACAAGCTGAGCCGCTCT 1275

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT37087

seq_documentation_block:
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ID   AAT37087 standard; cDNA to mRNA; 2064 BP.
XX
AC   AAT37087;
XX
DT   25-APR-1997 (first entry)
XX
DE   E1AF matrix metalloproteinase regulator, cDNA.
XX
KW   E1AF; matrix; metalloproteinase; regulator; infiltration; cancer;
KW   metastasis; cell; control; antisense; decoy; DNA binding region;
KW   target DNA; ribosome; induction; diagnosis; detection; treatment;
KW   mammary cancer; fibrosarcoma; osteosarcoma; lung cancer; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1389
FT                   /*tag= a
XX
PN   WO9624379-A1.
XX
PD   15-AUG-1996.
XX
PF   09-JAN-1996;   96WO-JP00016.
XX
PR   08-FEB-1995;   95JP-0020173.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
PI   Fujinaga K, Higashino F, Yoshida K;
XX
DR   WPI; 1996-384227/38.
DR   P-PSDB; AAW00167.
XX
PT   Control of cancer cell infiltration by E1AF gene expression
PT   regulation - also diagnosis of cancer by detection of E1AF gene
PT   expression products
XX
PS   Example 5; Pages 38-42; 65pp; Japanese.
XX
CC   The present sequence encodes the E1AF protein, which is a matrix
CC   metalloproteinase regulator. The infiltration and metastasis of
CC   cancer cells can be controlled by regulating the expression and
CC   expression products of the E1AF gene. This may be accomplished by
CC   inducing antisense DNA or RNA for the E1AF gene, a decoy gene
CC   expressing the DNA binding region of the E1AF protein, the target
CC   DNA for the DNA binding region of the E1AF protein or ribosomes
CC   corresponding to the E1AF gene mRNA. Cancer can be diagnosed by
CC   detecting E1AF gene expression products, e.g. E1AF protein or mRNA.
CC   These methods may be used in the treatment and diagnosis of cancer,
CC   e.g. mammary cancer, fibrosarcoma, osteosarcoma, lung cancer, etc..
XX
SQ   Sequence 2064 BP; 427 A; 648 C; 569 G; 420 T; 0 other;


alignment_scores:
            Quality:   14.00              Length:     14
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
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     294 LysAsnArgProAlaMetAsnTyrAspLysLeuSerArgSer 307
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    1087 AAGAACCGGCCAGCCATGAATTACGACAAGCTGAGCCGCTCG 1128

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ50016

seq_documentation_block:
ID   AAZ50016 standard; cDNA; 2064 BP.
XX
AC   AAZ50016;
XX
DT   25-APR-2000 (first entry)
XX
DE   Human polyomavirus enhancer activator 3 cDNA.
XX
KW   Human polyomavirus enhancer activator 3; PEA3; transformation;
KW   tumorigenic; metastatic; cancer; neu-mediated cancer; ovarian cancer;
KW   ras-mediated cancer; HER/neu promoter; anti-transformation therapy;
KW   anti-cancer therapy; cytostatic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1389
FT                   /*tag= a
FT                   /product= "Human polyomavirus enhancer activator 3"
XX
PN   WO200004153-A2.
XX
PD   27-JAN-2000.
XX
PF   15-JUL-1999;   99WO-US16142.
XX
PR   15-JUL-1998;   98US-0116049.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Hung M;
XX
DR   WPI; 2000-171269/15.
DR   P-PSDB; AAY44725.
XX
PT   Repression of cell transformation used to suppress tumor growth,
PT   comprises contacting the cell with human polyomavirus enhancer
PT   activator 3 -
XX
PS   Disclosure; Page 89; 92pp; English.
XX
CC   The patent discloses methods for repressing transformation in a cell by
CC   contacting it with polyomavirus enhancer activator 3 (PEA3) to inhibit a
CC   transformed phenotype resulting in reduced tumorigenic or metastatic
CC   potential of a cell. This is used in the treatment of various forms of
CC   cancer, e.g. neu- or ras- mediated cancers. The nucleic acid is
CC   introduced into the mammal through a vector or liposomal complex having
CC   DOTMA, DOPE or DC-Chol. The present cDNA sequence encodes human PEA3.
CC   Human PEA3 binds to a DNA element in the HER/neu promoter and represses
CC   transcription in HER2/neu-overexpressing ovarian cancer cells. This can
CC   be used in combination with anti-transformation/anti-cancer therapies or
CC   chemotherapeutic agents.
XX
SQ   Sequence 2064 BP; 427 A; 648 C; 569 G; 420 T; 0 other;


alignment_scores:
            Quality:   14.00              Length:     14
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAZ50016   ..

 Align seg 1/1  to: AAZ50016  from: 1  to: 2064

     294 LysAsnArgProAlaMetAsnTyrAspLysLeuSerArgSer 307
         |||||||||||||||||||||||||||||||||||||||||||
    1087 AAGAACCGGCCAGCCATGAATTACGACAAGCTGAGCCGCTCG 1128

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ55149

seq_documentation_block:
ID   AAQ55149 standard; cDNA to mRNA; 2073 BP.
```

```
XX
AC   AAQ55149;
XX
DT   11-JUL-1994  (first entry)
XX
DE   Adenovirus E1A-F gene.
XX
KW   Adenovirus; cancer; ets oncogene; HeLa cell; enhancer core sequence;
KW   methylation; ds.
XX
OS   Human adenovirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             844..1311
FT                   /*tag= a
FT                   /note= "Claimed sequence"
XX
PN   JP05328975-A.
XX
PD   14-DEC-1993.
XX
PF   02-JUN-1992;   92JP-0165453.
XX
PR   02-JUN-1992;   92JP-0165453.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
DR   WPI; 1994-021923/03.
DR   P-PSDB; AAR45451.
XX
PT   Novel E1A-F gene - for production of adenovirus E1A-F and cancer
PT   research
XX
PS   Claim 1; Page 6; 7pp; Japanese.
XX
CC   The adenovirus E1A-F gene contains a 473bp open reading frame. The
CC   clone comprising the coding sequence was isolated by screening
CC   a HeLa cell cDNA library.
XX
SQ   Sequence 2073 BP; 458 A; 635 C; 561 G; 418 T; 1 other;


alignment_scores:
           Quality:   14.00            Length:     14
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAQ55149   ..

 Align seg 1/1  to: AAQ55149  from: 1  to: 2073

     294 LysAsnArgProAlaMetAsnTyrAspLysLeuSerArgSer 307
         |||||||||||||||||||||||||||||||||||||||||||
    1009 AAGAACCGGCCAGCCATGAATTACGACAAGCTGAGCCGCTCG 1050

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV32688

seq_documentation_block:
ID   AAV32688 standard; cDNA; 2410 BP.
XX
AC   AAV32688;
XX
DT   20-OCT-1998  (first entry)
XX
DE   Polyomavirus PEA3 cDNA.
XX
KW   Polyomavirus enhancer activator; PEA3; tumour; suppressor; inhibitor;
KW   transformation; HER-2; neu promoter; metastasis; cancer; ss.
XX
OS   Polyomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             126..1793
FT                   /*tag= a
FT                   /product= PEA3
FT                   /note= "polyomavirus enhancer activator"
XX
PN   WO9830585-A2.
XX
PD   16-JUL-1998.
XX
PF   12-JAN-1998;   98WO-US00880.
XX
PR   10-JAN-1997;   97US-0780835.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Hung M,  Xing X;
XX
DR   WPI; 1998-399061/34.
DR   P-PSDB; AAW49010.
XX
PT   Method for repressing transformation of cells - by contacting cell
PT   with polyoma-virus enhancer activator 3, useful for, e.g. treating
PT   or preventing cancer, tumourigenesis and metastasis
XX
PS   Disclosure; Page 69-70; 83pp; English.
XX
CC   This sequence encodes a polyomavirus enhancer activator, PEA3. This
CC   sequence is used in a method for repressing transformation in a cell
CC   which involves contacting the cell with PEA3 to inhibit a transformed
CC   phenotype. This sequence can also be used in a method to suppress the
CC   growth of a tumour in a mammal comprising introducing to the mammal a
CC   PEA3-encoding nucleic acid where the expression of PEA3 in the mammal
CC   results in a decrease in the growth rate of the tumour. PEA3 can regulate
CC   the HER-2/neu promoter by transcriptional repression and acts as a tumour
CC   repressor. The PEA3 can be used for reducing a transforming,
CC   tumourogenic or metastatic potential of a cell. It can be used for the
CC   prevention and treatment of such transformation-driven events as cancer,
CC   tumourigenesis and metastasis.
XX
SQ   Sequence 2410 BP; 521 A; 744 C; 645 G; 500 T; 0 other;


alignment_scores:
           Quality:   14.00            Length:     14
             Ratio:  1.000              Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAV32688   ..

 Align seg 1/1  to: AAV32688  from: 1  to: 2410

     294 LysAsnArgProAlaMetAsnTyrAspLysLeuSerArgSer 307
         |||||||||||||||||||||||||||||||||||||||||||
    1491 AAGAACCGGCCAGCCATGAATTATGACAAGCTGAGCCGCTCG 1532

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ50015

seq_documentation_block:
ID   AAZ50015 standard; cDNA; 2410 BP.
XX
AC   AAZ50015;
XX
DT   25-APR-2000  (first entry)
XX
DE   Murine polyomavirus enhancer activator 3 cDNA.
XX
KW   Murine polyomavirus enhancer activator 3; PEA3; transformation;
KW   tumorigenic; metastatic; cancer; neu-mediated cancer; ovarian cancer;
KW   ras-mediated cancer; HER/neu promoter; anti-transformation therapy;
KW   anti-cancer therapy; cytostatic; ss.
XX
OS   Mus musculus.
```

```
XX
FH   Key             Location/Qualifiers
FT   CDS             126..1793
FT                   /*tag= a
FT                   /product= "Murine polyomavirus enhancer activator 3"
XX
PN   WO200004153-A2.
XX
PD   27-JAN-2000.
XX
PF   15-JUL-1999;   99WO-US16142.
XX
PR   15-JUL-1998;   98US-0116049.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Hung M;
XX
DR   WPI; 2000-171269/15.
DR   P-PSDB; AAY44724.
XX
PT   Repression of cell transformation used to suppress tumor growth,
PT   comprises contacting the cell with human polyomavirus enhancer
PT   activator 3 -
XX
PS   Disclosure; Page 86-87; 92pp; English.
XX
CC   The patent discloses methods for repressing transformation in a cell by
CC   contacting it with polyomavirus enhancer activator 3 (PEA3) to inhibit a
CC   transformed phenotype resulting in reduced tumorigenic or metastatic
CC   potential of a cell. This is used in the treatment of various forms of
CC   cancer, e.g. neu- or ras- mediated cancers. The nucleic acid is
CC   introduced into the mammal through a vector or liposomal complex having
CC   DOTMA, DOPE or DC-Chol. The present cDNA sequence encodes murine PEA3.
CC   Murine PEA3 binds directly to HER/neu promoter and represses
CC   transcription in HER2/neu-overexpressing ovarian cancer cells. This can
CC   be used in combination with anti-transformation/anti-cancer therapies or
CC   chemotherapeutic agents.
XX
SQ   Sequence 2410 BP; 521 A; 744 C; 645 G; 500 T; 0 other;


alignment_scores:
            Quality:   14.00              Length:     14
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAZ50015   ..

 Align seg 1/1  to: AAZ50015  from: 1  to: 2410

     294 LysAsnArgProAlaMetAsnTyrAspLysLeuSerArgSer 307
         ||||||||||||||||||||||||||||||||||||||||||
    1491 AAGAACCGGCCAGCCATGAATTATGACAAGCTGAGCCGCTCG 1532

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF54019

seq_documentation_block:
ID   AAF54019 standard; cDNA; 2410 BP.
XX
AC   AAF54019;
XX
DT   30-MAR-2001  (first entry)
XX
DE   Mouse PEA-3 protein-encoding cDNA, SEQ ID NO:13.
XX
KW   Age-related gene regulation; gene expression; human protein C; hPC;
KW   5' UTR; 5' untranslated region; age-regulatable expression construct;
KW   PEA-3 element; polyoma virus activator 3; antisense therapy;
KW   gene therapy; thrombosis; cardiovascular disease; diabetes;
KW   Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;
KW   ostcoarthritis; dementia; ss.
XX
OS   Mus musculus.
XX
PN   WO200075279-A2.
XX
PD   14-DEC-2000.
XX
PF   06-JUN-2000; 2000WO-US15728.
XX
PR   09-JUN-1999;   99US-0328925.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Kurachi K,  Kurachi S;
XX
DR   WPI; 2001-061708/07.
DR   P-PSDB; AAB60290.
XX
PT   New regulatory elements that control age-related gene expression,
PT   useful in gene therapy and for reducing Factor IX expression -
XX
PS   Disclosure; Fig 9A; 225pp; English.
XX
CC   The invention relates to nucleic acid sequences which regulate gene
CC   expression in an age-related manner and/or in a liver-specific manner.
CC   The invention identifies regions of the human factor IX (hFIX) gene, and
CC   a region of the human protein C (hPC) gene, which are age-related
CC   regulatory sequences. The hFIX age-related regulatory sequences are
CC   designated AE5' (AAF54016) and AE3' (AAF54017) and are found in the 5'
CC   UTR (at position 2164-2165 of AAF54018) and 3' UTR (at position
CC   34383-35655 of AAF54018) respectively. These elements act synergistically
CC   to increase hFIX levels over the lifespan of an individual; however, they
CC   can independently exert effects on hFIX mRNA in an age-related manner,
CC   with AE5' acting to stabilise hFIX mRNA, and AE3' acting to increase hFIX
CC   mRNA levels, over time. AE5' also directs liver-specific expression. The
CC   hPC gene age-related regulatory sequence is found in the 5' UTR
CC   (AAF54081), and contains two PEA-3 (polyoma virus activator 3) elements
CC   5'-GAGGAAA-3' and 5'-CAGGAAG-3'. The age-related regulatory sequences of
CC   the invention, along with their homologues, variants and fragments, may
CC   be used in the construction of recombinant expression vectors for the
CC   expression of a desired sequence in an age-related fashion in a host
CC   cell. Preferred target genes for expression in such age-regulatable
CC   expression vectors include those encoding proteins involved in blood
CC   coagulation (e.g., the pro-coagulants factor IX and factor VIII, and the
CC   anti-coagulants protein C and antithrombin III), human
CC   alpha-1-antitrypsin, PEA-3 protein and reporter proteins such as
CC   luciferase. Preferred promoters for use in such age-regulatable
CC   expression vectors include the human factor IX promoter, the T7 promoter,
CC   the T3 promoter and the SP6 promoter. The expression vectors of the
CC   invention may be used in gene therapy to provide age- related and/or
CC   liver-specific expression of target genes. Age-regulatable constructs may
CC   be used in the treatment of such age-related conditions such as
CC   thrombosis, cardiovascular disease, diabetes, Alzheimer's disease,
CC   Parkinson's disease, cancer, osteoporosis, osteoarthritis and dementia.
CC   Specifically, they may be used to express factor IX antisense mRNA in the
CC   treatment of thrombotic conditions associated with the natural
CC   age-related rise in factor IX expression. Transgenic cells or animals
CC   that contain vectors of the invention are useful as models of these
CC   diseases, in screening for potential therapeutic agents and for studying
CC   normal processes such as ageing and gene expression. Fragments and
CC   homologues of age-related regulatory sequences, are useful as probes to
CC   detect, isolate or identify other such sequences in samples. The present
CC   sequence represents a nucleic acid sequence which may be incorporated
CC   into a vector of the invention.
XX
SQ   Sequence 2410 BP; 521 A; 744 C; 645 G; 500 T; 0 other;


alignment_scores:
            Quality:   14.00              Length:     14
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000
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alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAF54019   ..

Align seg 1/1  to: AAF54019  from: 1  to: 2410

     294 LysAsnArgProAlaMetAsnTyrAspLysLeuSerArgSer 307
         |||||||||||||||||||||||||||||||||||||||||||
    1491 AAGAACCGGCCAGCCATGAATTATGACAAGCTGAGCCGCTCG 1532

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC99029

seq_documentation_block:
ID   AAC99029 standard; cDNA; 2952 BP.
XX
AC   AAC99029;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:257.
XX
KW   Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW   detection; diagnosis; identification; cytostatic; neuroprotective;
KW   nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW   antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW   linkage analysis; tissue identification; tissue typing; forensic;
KW   neural; immune system; muscular; reproductive; gastrointestinal;
KW   pulmonary; cardiovascular; renal; proliferative; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055320-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05989.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-579444/54.
DR   P-PSDB; AAB54264.
XX
PT   New nucleic acid that is a pancreatic cancer antigen for preventing,
PT   treating, or ameliorating a medical condition, particular pancreatic
PT   cancer, or for use in assays for diagnosing a pathological condition -
XX
PS   Claim 1; Page 696-697; 1379pp; English.
XX
CC   AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC   proteins, called pancreatic cancer antigens, given in AAB54008 to
CC   AAB54466. The human pancreatic cancer antigens have cytostatic,
CC   neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC   gynaecological, cardiant and antiinflammatory activities, and can be used
CC   in gene therapy. The polynucleotide and proteins can be used for
CC   preventing, treating, or ameliorating a medical condition or in assays
CC   for diagnosing a pathological condition or a susceptibility to one in a
CC   subject. Binding partners to the proteins and the activity of the
CC   proteins can be identified. The pancreatic cancer antigens can be used to
CC   detect, treat or prevent pancreatic disorders, especially cancer.
CC   Agonists and antagonists to the antigens can be screened for. The
CC   pancreatic cancer antigen polynucleotides can be used to design nucleic
CC   acid hybridisation probes that can be used in chromosome mapping, linkage
CC   analysis, tissue identification and/or typing and a variety of forensic
CC   and diagnostic methods. The proteins can be used to generate antibodies
CC   which are used to purify, detect and target the polypeptides, including
CC   both in vivo and in vitro diagnostic and therapeutic methods. The
CC   proteins can be used to treat or prevent neural, immune system, muscular,
CC   reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC   proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC   sequences used in the exemplification of the present invention.
XX
SQ   Sequence 2952 BP; 766 A; 645 C; 671 G; 868 T; 2 other;


alignment_scores:
          Quality:   14.00              Length:     14
            Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAC99029   ..

 Align seg 1/1  to: AAC99029  from: 1  to: 2952

     294 LysAsnArgProAlaMetAsnTyrAspLysLeuSerArgSer 307
         |||||||||||||||||||||||||||||||||||||||||||
     307 AAGAACCGGCCAGCCATGAACTATGACAAGCTGAGCCGCTCT 348

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF54723

seq_documentation_block:
ID   AAF54723 standard; DNA; 35465 BP.
XX
AC   AAF54723;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Nucleotide sequence of a human polynucleotide sequence.
XX
KW   Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW   ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW   neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW   Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW   rheumatoid polyarthritis; lupus erythematosus; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200105422-A2.
XX
PD   25-JAN-2001.
XX
PF   17-JUL-2000; 2000WO-FR02057.
XX
PR   15-JUL-1999;   99FR-0009372.
XX
PA   (INMR ) BIOMERIEUX STELHYS.
XX
PI   Roecklin D,  Kolbe H,  Charles M,  Malcus C,  Santoro L,  Perron H;
XX
DR   WPI; 2001-159475/16.
XX
PT   Detecting, preventing and treating degenerative, neurological and
PT   autoimmune diseases, particularly multiple sclerosis, using specified
PT   polypeptides or related nucleic acid or ligand -
XX
PS   Claim 11; Page 190-201; 209pp; French.
XX
CC   The present sequence represents a human polynucleotide sequence, which
CC   is used in the method of the invention. The specification describes a
CC   method which uses at least one polypeptide or polynucleotide sequence
CC   belonging to the perlecan, precursor of the retinol-binding plasma
CC   protein, precursor of the ganglioside GM2 activator, calgranulin B or
CC   saposin B protein families. The method is used for detecting,
CC   preventing or treating a degenerative, neurological and/or auto-immune
CC   disease. The polynucleotides and polypeptides are used for diagnosis,
CC   prognosis, prevention and treatment of multiple sclerosis (in its
CC   various forms and phases). They may also be useful in cases of
CC   e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,
CC   rheumatoid polyarthritis and lupus erythematosus, including use as
CC   vaccines and in gene therapy (expression of sense or antisense
CC   sequences). They can also be used to assess efficacy of potential
CC   therapeutic agents, particularly compounds that reduce or inhibit
CC   toxicity towards glial cells.
```

```
XX
SQ   Sequence 35465 BP; 8479 A; 9792 C; 8801 G; 8393 T; 0 other;


alignment_scores:
            Quality:   10.00              Length:     10
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAF54723/rev   ..

 Align seg 1/1  to reverse of: AAF54723  from: 1  to: 35465

       4 SerProGlyLeuSerSerValSerProSer 13
         ||||||||||||||||||||||||||||||
   28574 TCTCCGGGCCTCTCCTCCGTCTCCCCCTCC 28545

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV89617

seq_documentation_block:
ID   AAV89617 standard; cDNA; 261 BP.
XX
AC   AAV89617;
XX
DT   15-FEB-1999  (first entry)
XX
DE   EST clone CO334.
XX
KW   Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
KW   tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
KW   receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9845436-A2.
XX
PD   15-OCT-1998.
XX
PF   10-APR-1998;   98WO-US06955.
XX
PR   10-APR-1997;   97US-0838821.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1999-070077/06.
XX
PT   New polynucleotides encoding human secreted proteins - derived from
PT   e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT   ovary, pituitary, retina and colon cDNA libraries.
XX
PS   Claim 1; Page 275; 618pp; English.
XX
CC   The present sequence represents a human expressed sequence tag (EST).
CC   The polynucleotide, which is a secreted EST, and the encoded protein
CC   are predicted to have useful biological activities which would make
CC   them suitable for treating, preventing or ameliorating medical
CC   conditions in humans and animals, although no supporting data is
CC   given. Suggested activities include nutritional activity, immune
CC   stimulating or suppressing activity, haematopoiesis regulating
CC   activity, tissue growth activity, activin/inhibin activity,
CC   chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC   activity, receptor/ligand activity, anti-inflammatory activity,
CC   cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity. The polynucleotide may also be useful for gene therapy.
XX
SQ   Sequence 261 BP; 58 A; 80 C; 37 G; 86 T; 0 other;


alignment_scores:
            Quality:    9.00              Length:      9
              Ratio:  1.000                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-126-945B-2_COPY_2_335 x AAV89617   ..

 Align seg 1/1  to: AAV89617  from: 1  to: 261

      11 SerProSerHisLeuLeuLeuProPro 19
         |||||||||||||||||||||||||||
     101 TCTCCCAGCCATCTTCTACTGCCTCCC 127
```